	Type	L #	Hits	Search Text	DBs	Time Stamp	Comments	Error Definition	Errors
1	BRS	L1	121	phospholamban	USPAT; US-PGPUB; EPO; JPO; DERWENT	2003/08/11 17:43			0
2	BRS	L2	32	phospholamban same (deactivat$3 or bind$3)	USPAT; US-PGPUB; EPO; JPO; DERWENT	2003/08/11 17:44			0
3	BRS	L3	67	phospholamban same inhibit$3	USPAT; US-PGPUB; EPO; JPO; DERWENT	2003/08/11 17:45			0
4	BRS	L4	3158	cyclic adj peptide	USPAT; US-PGPUB; EPO; JPO; DERWENT	2003/08/11 17:46			0
5	BRS	L5	11900	(molecular adj model$3) or (computer adj model$3)	USPAT; US-PGPUB; EPO; JPO; DERWENT	2003/08/11 17:46			0
6	BRS	L6	0	5 same (2 or 3)	USPAT; US-PGPUB; EPO; JPO; DERWENT	2003/08/11 17:47			0
7	BRS	L7	1	4 same (2 or 3)	USPAT; US-PGPUB; EPO; JPO; DERWENT	2003/08/11 17:47			0
8	BRS	L8	1	(cytosolic adj domain) same phospholamban	USPAT; US-PGPUB; EPO; JPO; DERWENT	2003/08/11 17:51			0

	Type	L #	Hits	Search Text	DBs	Time Stamp	Comments	Error Definition	Errors
9	BRS	L9	4	caAtPase	USPAT; US-PGPUB; EPO; JPO; DERWENT	2003/08/11 17:51			0
10	BRS	L10	34	ca-AtPase	USPAT; US-PGPUB; EPO; JPO; DERWENT	2003/08/11 17:51			0
11	BRS	L11	2	(caAtPase or ca-AtPase) same phospholamban	USPAT; US-PGPUB; EPO; JPO; DERWENT	2003/08/11 17:52			0

FILE 'MEDLINE' ENTERED AT 18:02:07 ON 11 AUG 2003

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FILE 'AGRICOLA' ENTERED AT 18:02:07 ON 11 AUG 2003

=> s phospholamban
L1 5880 PHOSPHOLAMBAN

=> s l1 (p) (inhibit? or deactivat?)
L2 1548 L1 (P) (INHIBIT? OR DEACTIVAT?)

=> s cyclic peptide
L3 11269 CYCLIC PEPTIDE

=> s l2 (p) l3
L4 0 L2 (P) L3

=> s (molecular model?) or (computer model?)
L5 117423 (MOLECULAR MODEL?) OR (COMPUTER MODEL?)

=> s l2 (p) l5
L6 15 L2 (P) L5

=> duplicateremove l6
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KEEP DUPLICATES FROM MORE THAN ONE FILE? Y/(N):n
PROCESSING COMPLETED FOR L6
L7 5 DUPLICATE REMOVE L6 (10 DUPLICATES REMOVED)

=> d l7 1-15 ibib abs

L7 ANSWER 1 OF 5 CAPLUS COPYRIGHT 2003 ACS on STN
ACCESSION NUMBER: 2003:78629 CAPLUS
DOCUMENT NUMBER: 138:250620
TITLE: Modeling of the inhibitory interaction of phospholamban with the Ca2+ ATPase
AUTHOR(S): Toyoshima, Chikashi; Asahi, Michio; Sugita, Yuji; Khanna, Reena; Tsuda, Takeo; MacLennan, David H.
CORPORATE SOURCE: Institute of Molecular and Cellular Biosciences, University of Tokyo, Tokyo, 113-0032, Japan
SOURCE: Proceedings of the National Academy of Sciences of the United States of America (2003), 100(2), 467-472
CODEN: PNASA6; ISSN: 0027-8424
PUBLISHER: National Academy of Sciences
DOCUMENT TYPE: Journal
LANGUAGE: English
AB The inhibitory interaction of phospholamban (PLN) with the sarco(endo)plasmic reticulum Ca2+ ATPase isoform 1 (SERCA1a) was modeled on the basis of several constraints which included (i) spontaneous formation of SS-bridges between mutants L321C in transmembrane helix 4 (M4) of SERCA1a and N27C in PLN and between V89C (M4) and V49C (PLN); (ii) definition of the face of the PLN transmembrane helix that interacts with SERCA; (iii) crosslinking between Lys-3 of PLN and Lys-397 and Lys-400 of SERCA2a. The crystal structure of SERCA1a in the absence of Ca2+, which binds PLN, was used as the structure into which an at. model of PLN was built. PLN can fit into a transmembrane groove formed by the juxtaposition of M2, the upper part of M4, M6, and M9. In the SERCA1a structure with bound Ca2+, this groove is closed, accounting for the ability of Ca2+ to disrupt PLN-SERCA interactions. Near the cytoplasmic surface of the bilayer, the PLN helix is disrupted to prevent its collision with M4. The model can be extended into the cytoplasmic domain

so that Lys-3 in PLN can be cross-linked with Lys-397 and Lys-400 in SERCA1a with little unwinding of the N-terminal helix of PLN.

REFERENCE COUNT: 37 THERE ARE 37 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L7 ANSWER 2 OF 5 MEDLINE on STN DUPLICATE 1
ACCESSION NUMBER: 2001553881 MEDLINE
DOCUMENT NUMBER: 21486400 PubMed ID: 11477077
TITLE: Role of cysteine residues in structural stability and function of a transmembrane helix bundle.
AUTHOR: Karim C B; Paterlini M G; Reddy L G; Hunter G W; Barany G; Thomas D D
CORPORATE SOURCE: Departments of Biochemistry, Molecular Biology, and Biophysics, Medicinal Chemistry, University of Minnesota, Minneapolis, Minnesota 55455, USA.. cbk@ddt.biochem.umn.edu
CONTRACT NUMBER: 1K02 HL04209 (NHLBI)
DA0037 (NIDA)
GM27906 (NIGMS)
GM51628 (NIGMS)
SOURCE: JOURNAL OF BIOLOGICAL CHEMISTRY, (2001 Oct 19) 276 (42) 38814-9.
Journal code: 2985121R. ISSN: 0021-9258.
PUB. COUNTRY: United States
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 200112
ENTRY DATE: Entered STN: 20011016
Last Updated on STN: 20030105
Entered Medline: 20011204

AB To study the structural and functional roles of the cysteine residues at positions 36, 41, and 46 in the transmembrane domain of ***phospholamban*** (PLB), we have used Fmoc (N-(9-fluorenyl)methoxycarbonyl) solid-phase peptide synthesis to prepare alpha-amino-n-butyric acid (Abu)-PLB, the analogue in which all three cysteine residues are replaced by Abu. Whereas previous studies have shown that replacement of the three Cys residues by Ala (producing Ala-PLB) greatly destabilizes the pentameric structure, we hypothesized that replacement of Cys with Abu, which is isosteric to Cys, might preserve the pentameric stability. Therefore, we compared the oligomeric structure (from SDS-polyacrylamide gel electrophoresis) and function (***inhibition*** of the Ca-ATPase in reconstituted membranes) of Abu-PLB with those of synthetic wild-type PLB and Ala-PLB. ***Molecular*** ***modeling*** provides structural and energetic insight into the different oligomeric stabilities of these molecules. We conclude that 1) the Cys residues of PLB are not necessary for pentamer formation or ***inhibitory*** function; 2) the steric properties of cysteine residues in the PLB transmembrane domain contribute substantially to pentameric stability, whereas the polar or chemical properties of the sulfhydryl group play only a minor role; 3) the functional potency of these PLB variants does not correlate with oligomeric stability; and 4) acetylation of the N-terminal methionine has neither a functional nor a structural effect in full-length PLB.

L7 ANSWER 3 OF 5 CAPLUS COPYRIGHT 2003 ACS on STN
ACCESSION NUMBER: 2001:34634 CAPLUS
DOCUMENT NUMBER: 134:218589
TITLE: Reexamination of the role of the leucine/isoleucine zipper residues of phospholamban in inhibition of the Ca2+ pump of cardiac sarcoplasmic reticulum
AUTHOR(S): Cornea, Razvan L.; Autry, Joseph M.; Chen, Zhenhui; Jones, Larry R.
CORPORATE SOURCE: Department of Medicine and the Krannert Institute of Cardiology, Indiana University School of Medicine, Indianapolis, IN, 46202, USA
SOURCE: Journal of Biological Chemistry (2000), 275(52), 41487-41494
CODEN: JBCHA3; ISSN: 0021-9258
PUBLISHER: American Society for Biochemistry and Molecular Biology
DOCUMENT TYPE: Journal
LANGUAGE: English

AB Phospholamban is a small phosphoprotein inhibitor of the Ca2+-pump in cardiac sarcoplasmic reticulum, which shows a distinct oligomeric distribution between monomers and homopentamers that are stabilized through Leu/Ile zipper interactions. A two-faced model of phospholamban inhibition of the Ca2+-pump was proposed, in which the Leu/Ile zipper

residues located on one face of the transmembrane .alpha.-helix regulate the pentamer to monomer equ[illegible], whereas residues on the othe[illegible]face of the helix bind to and inhibit the pump. Here we tested this two-faced model of phospholamban action by analyzing the functional effects of a new series of Leu/Ile zipper mutants. Pentameric stabilities of the mutants were quantified at different SDS concns. We show that several phospholamban mutants with hydrophobic amino acid substitutions at the Leu/Ile zipper region retain the ability to form pentamers but at the same time give the same or even stronger (i.e. L37I-PLB) inhibition of the Ca2+-pump than do mutants that are more completely monomeric. Steric constraints prevent the Leu/Ile zipper residues sequestered in the interior of the phospholamban pentamer from binding to the Ca2+-pump, leading to the conclusion that the zipper residues access the pump from the phospholamban monomer, which is the active inhibitory species. A modified model of phospholamban transmembrane domain action is proposed, in which the membrane span of the phospholamban monomer maintains contacts with the Ca2+-pump around most of its circumference, including residues located in the Leu/Ile zipper region.

REFERENCE COUNT: 25 THERE ARE 25 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L7 ANSWER 4 OF 5 MEDLINE on STN DUPLICATE 2

ACCESSION NUMBER: 2000071613 MEDLINE
DOCUMENT NUMBER: 20071613 PubMed ID: 10603946
TITLE: Direct spectroscopic detection of molecular dynamics and interactions of the calcium pump and phospholamban.
AUTHOR: Thomas D D; Reddy L G; Karim C B; Li M; Cornea R; Autry J M; Jones L R; Stamm J
CORPORATE SOURCE: Department of Biochemistry, University of Minnesota Medical School, Minneapolis 55455, USA.. ddt@ddt.biochem.umn.edu
CONTRACT NUMBER: GM27906 (NIGMS)
HL06308 (NHLBI)
HL49428 (NHLBI)
SOURCE: ANNALS OF THE NEW YORK ACADEMY OF SCIENCES, (1998 Sep 16) 853 186-94. Ref: 23
Journal code: 7506858. ISSN: 0077-8923.
PUB. COUNTRY: United States
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
General Review; (REVIEW)
(REVIEW, TUTORIAL)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 200001
ENTRY DATE: Entered STN: 20000124
Last Updated on STN: 20000124
Entered Medline: 20000107

AB In order to test ***molecular*** ***models*** of cardiac calcium transport regulation, we have used spectroscopy to probe the structures, dynamics, and interactions of the Ca pump (Ca-ATPase) and ***phospholamban*** (PLB) in cardiac sarcoplasmic reticulum (SR) and in reconstituted membranes. Electron paramagnetic resonance (EPR) and phosphorescence of probes bound to the Ca pump show that the activity of the pump is quite sensitive to its oligomeric interactions. In cardiac SR, PLB aggregates and ***inhibits*** the pump, and both effects are reversed by PLB phosphorylation. Previous analyses of PLB's oligomeric state were only in detergent solutions, so we used EPR and fluorescence to determine the oligomeric structure of PLB in its native state in lipid bilayers. Wild-type PLB is primarily oligomeric in the membrane, while the mutant L37A-PLB is monomeric. For both proteins, phosphorylation shifts the dynamic monomer-oligomer equilibrium toward oligomers, and induces a similar structural change, as indicated by tyrosine fluorescence; yet L37A-PLB is more effective than wild-type PLB in ***inhibiting*** and aggregating the pump. Fluorescence energy transfer shows that the Ca pump increases the fraction of monomeric PLB, indicating that the pump preferentially binds monomeric PLB. These results support a reciprocal aggregation model for Ca pump regulation, in which the Ca pump is aggregated and ***inhibited*** by association with PLB monomers, and phosphorylation of PLB reverses these effects while decreasing the concentration of PLB monomers. To investigate the structure of the PLB pentamer in more detail, we measured the reactivities of cysteine residues in the transmembrane domain of PLB, and recorded EPR spectra of spin labels attached to these sites. These results support an atomic structural model, based on molecular dynamics simulations and mutagenesis studies, in which the PLB pentamer is stabilized by a leucine-isoleucine zipper within the transmembrane domain.

L7 ANSWER 5 OF 5 MEDLINE on STN DUPLICATE 3

ACCESSION NUMBER: 95271668 MEDLINE
DOCUMENT NUMBER: 95271668 PubMed ID: 7752243
TITLE: Structural model of the phospholamban ion channel complex in phospholipid membranes.
AUTHOR: Arkin I T; Rothman M; Ludlam C F; Aimoto S; Engelman D M; Rothschild K J; Smith S O
CORPORATE SOURCE: Department of Cell Biology, Yale University School of Medicine, New Haven, CT 06510, USA.
CONTRACT NUMBER: GM 22778 (NIGMS)
GM 46732 (NIGMS)
GM 47527 (NIGMS)
SOURCE: JOURNAL OF MOLECULAR BIOLOGY, (1995 May 12) 248 (4) 824-34.
Journal code: 2985088R. ISSN: 0022-2836.
PUB. COUNTRY: ENGLAND: United Kingdom
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 199506
ENTRY DATE: Entered STN: 19950629
Last Updated on STN: 19950629
Entered Medline: 19950620

AB ***Phospholamban*** is a 52 amino acid residue membrane protein involved with the regulation of calcium levels across sarcoplasmic reticulum membranes in cardiac muscle cells. The N-terminal 30 amino acid residues of the protein are largely hydrophilic and include two sites whose phosphorylation is thought to dissociate an ***inhibitory*** complex between ***phospholamban*** and Ca2+ ATPase. The C-terminal 22 amino acid residues are largely hydrophobic, anchor the protein in the membrane and are responsible for Ca2+ selective ion conductance. Specific interactions between the transmembrane domains stabilize a pentameric protein complex. We have obtained circular dichroism (CD), transmission Fourier transform infrared (FTIR) and attenuated total reflection Fourier transform infrared (ATR-FTIR) spectra of the full-length protein and have compared these results to those from a 28 residue peptide that includes the transmembrane domain. Both proteins reconstituted into phospholipid membranes are largely alpha-helical by CD and FTIR. Polarized ATR-FTIR measurements show that both the cytosolic and transmembrane helices are oriented perpendicular to the membrane plane with a tilt of 28 (+/- 6) degrees with respect to the membrane normal. This tilt angle is in close agreement to that calculated from a model for the transmembrane domain of ***phospholamban*** suggested by mutagenesis and ***molecular*** ***modeling*** . Phosphorylation does not significantly change the secondary structure or orientation of the protein. The pentameric complex is modeled as a left-handed coiled-coil of five long helices (40 (+/- 3) residues) that extend across the membrane from the lumenal carboxy terminus to the phosphorylation site in the cytoplasm. The helix bundle forms a perpendicular ion pore that may begin at a distance (17 to 29 A) from the membrane surface. Based on the above, we propose a mechanism by which ***phospholamban*** regulates Ca2+ levels across membranes that takes into account both its selective ion conductance and ***inhibitory*** association with the Ca2+ pump.

=> d his

(FILE 'HOME' ENTERED AT 18:01:45 ON 11 AUG 2003)

FILE 'MEDLINE, CAPLUS, BIOSIS, EMBASE, SCISEARCH, AGRICOLA' ENTERED AT 18:02:07 ON 11 AUG 2003
L1 5880 S PHOSPHOLAMBAN
L2 1548 S L1 (P) (INHIBIT? OR DEACTIVAT?)
L3 11269 S CYCLIC PEPTIDE
L4 0 S L2 (P) L3
L5 117423 S (MOLECULAR MODEL?) OR (COMPUTER MODEL?)
L6 15 S L2 (P) L5
L7 5 DUPLICATE REMOVE L6 (10 DUPLICATES REMOVED)

=> s cytosolic domain
L8 2126 CYTOSOLIC DOMAIN

=> s l8 (p) l1
L9 16 L8 (P) L1

=> s l9 (p) l2
L10 7 L9 (P) L2

=> duplicate remove l10

DUPLICATE PREFERENCE IS 'MEDLINE, CAPLUS, BIOSIS, EMBASE, SCISEARCH'
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PROCESSING COMPLETED FOR L10
L11 3 DUPLICATE REMOVE L10 (4 DUPLICATES REMOVED)

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L12 3 L11 NOT L7

=> d l12 1-3 ibib abs

L12 ANSWER 1 OF 3 MEDLINE on STN
ACCESSION NUMBER: 91329371 MEDLINE
DOCUMENT NUMBER: 91329371 PubMed ID: 1831047
TITLE: Phospholamban is related to the autoinhibitory domain of the plasma membrane Ca(2+)-pumping ATPase.
AUTHOR: Chiesi M; Vorherr T; Falchetto R; Waelchli C; Carafoli E
CORPORATE SOURCE: Department of Research, Pharmaceuticals Division, CIBA-GEIGY Limited, Basel, Switzerland.
SOURCE: BIOCHEMISTRY, (1991 Aug 13) 30 (32) 7978-83.
Journal code: 0370623. ISSN: 0006-2960.
PUB. COUNTRY: United States
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 199109
ENTRY DATE: Entered STN: 19911006
Last Updated on STN: 19970203
Entered Medline: 19910913
AB The Ca2+ pumps of the plasma membrane (PM ATPase) and of sarcoplasmic reticulum (SR ATPase) share a number of structural and functional properties. A major difference is the regulatory mechanism. The PM ATPase contains a C-terminal autoinhibitory domain; calmodulin binds to it, removing the ***inhibition*** . The SR ATPase contains a domain that interacts with the ***inhibitor*** protein ***phospholamban*** when the latter is in the nonphosphorylated state; phosphorylation of ***phospholamban*** removes the ***inhibition*** . Peptides corresponding to the autoinhibitory domain of the PM ATPase were synthesized and found to ***inhibit*** the SR ATPase. A 28-residue peptide (C28W), containing the entire autoinhibitory domain, was the most powerful (IC50 = 15 microM; lmax greater than 90%). The ***inhibition*** was Ca2+ dependent and more pronounced at submicromolar Ca2+ concentrations. C28W is about 50% homologous to the ***cytosolic*** ***domain*** of ***phospholamban*** , the hydrophilic portion of which was found to interact directly with calmodulin (Kd = about 700 nM). However, while calmodulin reversed the ***inhibition*** of the SR ATPase by C28W, it failed to reverse that induced by nonphosphorylated ***phospholamban*** .

L12 ANSWER 2 OF 3 CAPLUS COPYRIGHT 2003 ACS on STN
ACCESSION NUMBER: 2003:235489 CAPLUS
DOCUMENT NUMBER: 138:267695
TITLE: ***Phospholamban*** ***cytosolic*** ***domain*** structure determined by NMR and its use in rational design of ***inhibitors*** of the ATPase activity of the enzyme
INVENTOR(S): Pollesello, Piero; Ovaska, Martti; Tenhunen, Jukka; Vidgren, Jukka; Yliperttula-Ikonen, Marjo; Tilgmann, Carola; Lotta, Timo; Kaivola, Juha
PATENT ASSIGNEE(S): Orion Corporation, Finland
SOURCE: U.S., 58 pp., Cont.-in-part of U.S. Ser. No. 937,117, abandoned.
CODEN: USXXAM
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
US 6538022	B1	20030325	US 1999-252063	19990218
PRIORITY APPLN. INFO.:			US 1997-937117 B2	19970924

OTHER SOURCE(S): MARPAT 138:267695
AB The three-dimensional structure of the ***cytosolic*** ***domain*** of ***phospholamban*** (PLB) including the ATPase active site detd. from high resoln. NMR data. The structural information can be used in the rational design of of ***phospholamban*** ***inhibitors*** . Criteria for design of ligands and the synthesis of candidate compds. are

reported. Several of these compds. relieved the ***phospholamban*** ***inhibition*** of calcium uptake by vesicles of the sarcoplasmic reticulum of cardiac muscle.

REFERENCE COUNT: 31 THERE ARE 31 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L12 ANSWER 3 OF 3 SCISEARCH COPYRIGHT 2003 THOMSON ISI on STN
ACCESSION NUMBER: 91:455981 SCISEARCH
THE GENUINE ARTICLE: GA940
TITLE: PHOSPHOLAMBAN IS RELATED TO THE AUTOINHIBITORY DOMAIN OF THE PLASMA-MEMBRANE CA2+-PUMPING ATPASE
AUTHOR: CHIESI M; VORHERR T; FALCHETTO R; WAELCHLI C; CARAFOLI E (Reprint)
CORPORATE SOURCE: CIBA GEIGY AG, DEPT RES, DIV PHARMACEUT, CH-4002 BASEL, SWITZERLAND; SWISS FED INST TECHNOL, DEPT BIOCHEM, CH-8092 ZURICH, SWITZERLAND
COUNTRY OF AUTHOR: SWITZERLAND
SOURCE: BIOCHEMISTRY, (1991) Vol. 30, No. 32, pp. 7978-7983.
DOCUMENT TYPE: Article; Journal
FILE SEGMENT: LIFE
LANGUAGE: ENGLISH
REFERENCE COUNT: 30

ABSTRACT IS AVAILABLE IN THE ALL AND IALL FORMATS

AB The Ca2+ pumps of the plasma membrane (PM ATPase) and of sarcoplasmic reticulum (SR ATPase) share a number of structural and functional properties. A major difference is the regulatory mechanism. The PM ATPase contains a C-terminal autoinhibitory domain; calmodulin binds to it, removing the ***inhibition*** . The SR ATPase contains a domain that interacts with the ***inhibitor*** protein ***phospholamban*** when the latter is in the nonphosphorylated state; phosphorylation of ***phospholamban*** removes the ***inhibition*** . Peptides corresponding to the autoinhibitory domain of the PM ATPase were synthesized and found to ***inhibit*** the SR ATPase. A 28-residue peptide (C28W), containing the entire autoinhibitory domain, was the most powerful (IC50 = 15-mu-M; I(max) > 90%). The ***inhibition*** was Ca2+ dependent and more pronounced at submicromolar Ca2+ concentrations. C28W is about 50% homologous to the ***cytosolic*** ***domain*** of ***phospholamban*** , the hydrophilic portion of which was found to interact directly with calmodulin (K(d) = about 700 nM). However, while calmodulin reversed the ***inhibition*** of the SR ATPase by C28W, it failed to reverse that induced by nonphosphorylated ***phospholamban*** .

=> s miller allan/au
L13 5 MILLER ALLAN/AU

=> s treco douglas/au
L14 23 TRECO DOUGLAS/AU

=> s selden richard/au
L15 7 SELDEN RICHARD/AU

=> s (l13 or l14 or l15) and l1
L16 0 (L13 OR L14 OR L15) AND L1

=> d his

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FILE 'MEDLINE, CAPLUS, BIOSIS, EMBASE, SCISEARCH, AGRICOLA' ENTERED AT 18:02:07 ON 11 AUG 2003
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L2 1548 S L1 (P) (INHIBIT? OR DEACTIVAT?)
L3 11269 S CYCLIC PEPTIDE
L4 0 S L2 (P) L3
L5 117423 S (MOLECULAR MODEL?) OR (COMPUTER MODEL?)
L6 15 S L2 (P) L5
L7 5 DUPLICATE REMOVE L6 (10 DUPLICATES REMOVED)
L8 2126 S CYTOSOLIC DOMAIN
L9 16 S L8 (P) L1
L10 7 S L9 (P) L2
L11 3 DUPLICATE REMOVE L10 (4 DUPLICATES REMOVED)
L12 3 S L11 NOT L7
L13 5 S MILLER ALLAN/AU
L14 23 S TRECO DOUGLAS/AU
L15 7 S SELDEN RICHARD/AU

L16 0 S (L13 OR L14 OR L15) AND L1

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"HELP COMMANDS" at an arrow prompt (=>).

=> log y

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